

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/811,353  
Source: TFW  
Date Processed by STIC: 2-4-05

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IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/10/811,353

**DATE:** 02/04/2005  
**TIME:** 16:22:33

**Input Set :** A:\sequence.listing.ST25.txt  
**Output Set:** N:\CRF4\02042005\J811353.raw

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3 <110> APPLICANT: McCray, Paul B.
4      Sanders, David A.
5      Jeffers, Scott A.
6      Davidson, Beverly L.
7      Sinn, Patrick L.
9 <120> TITLE OF INVENTION: PSEUDOTYPED VIRUSES AND METHODS FOR THEIR USE
11 <130> FILE REFERENCE: 290.00670120
13 <140> CURRENT APPLICATION NUMBER: US 10/811,353
14 <141> CURRENT FILING DATE: 2004-03-26
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 681
22 <212> TYPE: PRT
23 <213> ORGANISM: Marburg virus glycoprotein
25 <400> SEQUENCE: 1
27 Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
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31 Lys Asn Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
32           20          25          30
35 Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
36           35          40          45
39 Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
40           50          55          60
43 Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
44 65           70          75          80
47 Val Glu Tyr Thr Glu Gly Glu Ala Lys Thr Cys Tyr Asn Ile Ser
48           85          90          95
51 Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
52           100         105         110
55 Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
56           115         120         125
59 Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
60           130         135         140
63 Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
64 145           150         155         160
67 Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
68           165         170         175
71 Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
72           180         185         190
75 Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
76           195         200         205
79 Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln

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80	210	215	220
83	Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro		
84	225	230	235
87	Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr		
88	245	250	255
91	Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly		
92	260	265	270
95	Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln		
96	275	280	285
99	Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr		
100	300	295	300
103	Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr		
104	305	310	315
107	320	315	320
108	Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His		
111	325	330	335
112	Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser		
115	340	345	350
116	Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser		
119	355	360	365
120	Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu		
123	370	375	380
124	Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys		
127	385	390	395
128	Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser		
131	405	410	415
132	Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg		
135	420	425	430
136	Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu		
139	435	440	445
140	Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr		
143	450	455	460
144	Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu		
147	465	470	475
148	Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro		
151	485	490	495
152	Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys		
155	500	505	510
156	Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala		
159	515	520	525
160	Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr		
163	530	535	540
164	Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg		
167	545	550	555
168	Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val		
171	565	570	575
172	Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp		
175	580	585	590
176	Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp		
	595	600	605

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179 Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile  
 180 610 615 620  
 183 Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu  
 184 625 630 635 640  
 187 Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly  
 188 645 650 655  
 191 Ile Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile  
 192 660 665 670  
 195 Cys Arg Ile Phe Thr Lys Tyr Ile Gly  
 196 675 680

199 &lt;210&gt; SEQ ID NO: 2

200 &lt;211&gt; LENGTH: 2046

201 &lt;212&gt; TYPE: DNA

202 &lt;213&gt; ORGANISM: Marburg virus glycoprotein

204 &lt;400&gt; SEQUENCE: 2

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207 atttagaga	tagctagtaa	caatcaaccc	caaaaatgtgg	attcggtatg	ctccggaaact	120
209 ctccagaaga	cagaagatgt	ccatctgtatg	ggattcacac	tgagtggca	aaaagttgt	180
211 gattcccctt	tggaggcattc	caagcgatgg	gcttcagga	caggtgtacc	tcccaagaat	240
213 gttagtata	cagaagggga	ggaagccaaa	acatgctaca	atataagtgt	aacggatccc	300
215 tctggaaaat	ccttgcgttt	ggatcctcct	accaacatcc	gtgactatcc	taaatgcaaa	360
217 actatccatc	atattcaagg	tcaaaacctt	catgcgaag	ggatgcctt	ccatttgtgg	420
219 ggagcatttt	tcctgtatga	tcgcattgcc	tccacaacaa	tgtaccgagg	cagagtcttc	480
221 actgaagggg	acatagcagc	tatgattgtc	aataagacag	tgcacaaaaat	gatttctcg	540
223 agcaggac	aggggtaccg	tcacatgaat	ctgacttcta	ctaataaata	ttggacaagt	600
225 aacaatggaa	cacaacgaa	tgacactgaa	tgcttcgggt	ctcttcaaga	atacaactcc	660
227 acgaagaatc	aaacatgtgc	tccgtccaaa	ataccctcac	cactgcccac	agcccggtcca	720
229 gagatcaaac	ccacaagcac	cccaactgtat	gccaccacac	tcaacaccac	agacccaaac	780
231 aatgatgatg	aggacccat	aacatccgtt	tcagggtccg	gagaacagga	accctatac	840
233 acttcagatg	cggtcactaa	gcaaggggctt	tcatcaacaa	tgccaccac	tccctcacca	900
235 caaccaagca	cggccacagca	agaagggaaac	aacacagacc	attcccaagg	tactgtgact	960
237 gaacccaaca	aaaccaacac	aacggcaca	ccgtccatgc	ccccccacaa	caccactgca	1020
239 atctctacta	acaacacctc	caagaacaaac	ttcagcaccc	tctctgtatc	actacaaaac	1080
241 accaccaatt	acgacacaca	gagcacagcc	actggaaatg	aacaaaccag	tgccccctcg	1140
243 aaacacaaccc	tgcctccaaac	aggaaatctt	accacagcaa	agagcactaa	caacacgaaa	1200
245 gggcccccca	caacggcacc	aaatatgaca	aatgggcatt	taaccagtcc	ctccccccacc	1260
247 cccaaacccga	ccacacaaca	tcttgatata	ttcagaaaga	aacgaagtat	cctctggagg	1320
249 gaaggcgaca	tgtttctttt	tctggacggg	ttaataatg	ctccaattga	ttttgatcca	1380
251 gttccaaata	caaagacat	ctttgatgaa	tcttctgtat	ctgggtctc	ggctgaggaa	1440
253 gatcaacatg	cctcccccaa	tatcagtta	actttatcct	atttcttaa	tataaatgaa	1500
255 aacactgcct	actctggaga	aatgagaac	gattgtatg	cagagttaag	aatttggagc	1560
257 gtcaggagg	atgacctggc	agcaggggctc	agttggatac	cgtttttgg	ccctggaaatc	1620
259 gaaggacttt	atactgctgg	ttaattaaa	aacccaaacaa	atttggtctg	caggttgagg	1680
261 cgtctagcca	atcaaactgc	caaattcctg	gaactcttat	taagagtcc	aaccgaggaa	1740
263 aggacatttt	ccttaattaa	tagacatgcc	attgacttcc	tactcacaag	gtggggagga	1800
265 acatgcaaag	tgcttgacc	tgattgttgc	attgaaatag	aagacttgc	caggaatatt	1860
267 tcggaacaaa	ttgaccaat	caaaaaagat	gaacaaaaag	aggggactgg	ttggggtcta	1920
269 ggtggtaaat	ggtgacatc	cgactgggt	gttctacta	acttggccat	tttgctacta	1980
271 ttatccatag	ctgtcttgc	tgtatgtc	gtatcttac	caaataatatc		2040

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Input Set : A:\sequence.listing.ST25.txt  
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273 gggtaa 2046  
 276 <210> SEQ ID NO: 3  
 277 <211> LENGTH: 676  
 278 <212> TYPE: PRT  
 279 <213> ORGANISM: Ebola virus glycoprotein  
 281 <400> SEQUENCE: 3  
 283 Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg  
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 287 Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser  
 288 20 25 30  
 291 Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val  
 292 35 40 45  
 295 Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg  
 296 50 55 60  
 299 Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro  
 300 65 70 75 80  
 303 Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val  
 304 85 90 95  
 307 Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu  
 308 100 105 110  
 311 Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly  
 312 115 120 125  
 315 Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr  
 316 130 135 140  
 319 Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe  
 320 145 150 155 160  
 323 Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe  
 324 165 170 175  
 327 Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp  
 328 180 185 190  
 331 Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp  
 332 195 200 205  
 335 Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly  
 336 210 215 220  
 339 Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr  
 340 225 230 235 240  
 343 Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu  
 344 245 250 255  
 347 Asn Glu Thr Arg Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys  
 348 260 265 270  
 351 Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp  
 352 275 280 285  
 355 Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu  
 356 290 295 300  
 359 Glu Leu Ser Phe Thr Ala Val Ser Asn Arg Ala Lys Asn Ile Ser Gly  
 360 305 310 315 320  
 363 Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr  
 364 325 330 335  
 367 Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln

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368	340	345	350
371	Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu		
372	355	360	365
375	Ala Thr Ile Ser Thr Ser Leu Arg Pro Pro Ile Thr Lys Pro Gly Pro		
376	370	375	380
379	Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu		
380	385	390	395
383	390	395	400
384	Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Ala Ser Thr		
387	405	410	415
388	420	425	430
391	425	430	
392	Glu Asn Thr Asn Thr Ser Lys Gly Thr Asp Leu Leu Asp Pro Ala Thr		
395	435	440	445
396	445	450	
399	450	455	460
400	His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly		
403	465	470	475
404	475	480	
407	Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly		
408	485	490	495
411	Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn		
412	500	505	510
415	Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly		
416	515	520	525
419	520	525	
420	Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile		
423	530	535	540
424	535	540	
427	Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln		
428	545	550	555
431	555	560	
432	Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr		
435	565	570	575
436	570	575	
439	Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe		
440	580	585	590
443	585	590	
444	Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys		
447	595	600	605
448	600	605	
451	Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp		
452	610	615	620
455	615	620	
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458	635	640	
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461	<211> LENGTH: 2030		
462	<212> TYPE: DNA		
463	<213> ORGANISM: Ebola virus glycoprotein		
464	<400> SEQUENCE: 4		
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**VERIFICATION SUMMARY** DATE: 02/04/2005  
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